

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/526,569A
Source: IFWP
Date Processed by STIC: 8/4/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/526,569A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWP

RAW SEQUENCE LISTING

DATE: 08/04/2006

PATENT APPLICATION: US/10/526,569A

TIME: 12:09:34

Input Set : A:\SAEG129.010APC.txt

Output Set: N:\CRF4\08042006\J526569A.raw

3 <110> APPLICANT: Yoshihiro OHMIYA, EMIKO ASHIDAKA and Seiji ITO
 5 <120> TITLE OF INVENTION: Secreted or membrane-binding chimeric protein
 7 <130> FILE REFERENCE: 200521/US
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/526,569A
 C--> 9 <141> CURRENT FILING DATE: 2005-03-04
 9 <160> NUMBER OF SEQ ID NOS: 10
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2388
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: fused gene consisting of Vargula Luciferase, yellow
 fluorescence
 20 protein from Aequorea and a DNA coding for spacer peptide
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(2388)
 25 <223> OTHER INFORMATION:
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 29 Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp
 30 1 5 10 15
 32 aac tgt caa gat gca tgt cct gta gaa gcg gaa ccg cca tca agt aca 96
 33 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr
 34 20 25 30
 36 cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat 144
 37 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
 38 35 40 45
 40 acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt 192
 41 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
 42 50 55 60
 44 gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gtg att 240
 45 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
 46 65 70 75 80
 48 gaa tgc aga gta gaa gca gct ggt tat ttt aga acg ttt tac ggc aaa 288
 49 Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys
 50 85 90 95
 52 aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct agg gga acc 336
 53 Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
 54 100 105 110
 56 aag ggt ggc gat tgg tct gta acc ctc acc atg gag aat cta gat gga 384
 57 Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
 58 115 120 125

**Does Not Comply
 Corrected Diskette Needed**

see p. 4

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Input Set : A:\SAEG129.010APC.txt

Output Set: N:\CRF4\08042006\J526569A.raw

60	cag aag gga gct gtg ctg act aag aca aca ctg gag gtt gca gga gac	432
61	Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp	
62	130 135 140	
64	gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga	480
65	Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly	
66	145 150 155 160	
68	gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc	528
69	Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr	
70	165 170 175	
72	att gct gtt gtt gaa ata ccg ggc ttc aat atc aca gtc atc gaa ttc	576
73	Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe	
74	180 185 190	
76	ttt aaa cta atc gtg att gat att ctg gga gga aga tct gtg aga att	624
77	Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile	
78	195 200 205	
80	gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat	672
81	Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn	
82	210 215 220	
84	ctg gag atg aat gac gct gat gac ttt act aca gat gca gat cag ctg	720
85	Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu	
86	225 230 235 240	
88	gcg atc caa ccc aac ata aac aaa gag ttc gac ggc tgc cca ttc tat	768
89	Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr	
90	245 250 255	
92	ggc aat cct tct gat atc gaa tac tgc aaa ggt ctg atg gag cca tac	816
93	Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr	
94	260 265 270	
96	aga gct gta tgt cgt aac aat atc aac ttc tac tat tac act cta tcc	864
97	Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Thr Leu Ser	
98	275 280 285	
100	tgt gcc ttc gct tac tgt atg gga gga gaa gaa aga gct aaa cac gtc	912
101	Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val	
102	290 295 300	
104	ctt ttc gac tat gtt gag aca tgc gct gcg ccg gaa acg aga gga acg	960
105	Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr	
106	305 310 315 320	
108	tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gca aga	1008
109	Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg	
110	325 330 335	
112	tat caa ttc cag ggc cca tgc aag gag att ctg atg gcc gca gac tgt	1056
113	Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys	
114	340 345 350	
116	tac tgg aac aca tgg gat gta aag gtt tca cat aga gac gtc gaa tca	1104
117	Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser	
118	355 360 365	
120	tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta	1152
121	Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val	
122	370 375 380	
124	gat ctc att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta	1200

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126	385					390					395					400	
128	tct	atc	ccg	tac	agc	tct	gag	aac	act	tcc	ata	tac	tgg	cag	gat	gga	1248
129	Ser	Ile	Pro	Tyr	Ser	Ser	Glu	Asn	Thr	Ser	Ile	Tyr	Trp	Gln	Asp	Gly	
130					405				410					415			
132	gac	atc	ctg	acg	acg	gcc	atc	cta	cct	gaa	gct	ctt	gtc	gtt	aag	ttc	1296
133	Asp	Ile	Leu	Thr	Thr	Ala	Ile	Leu	Pro	Glu	Ala	Leu	Val	Val	Lys	Phe	
134				420				425					430				
136	aac	ttt	aag	cag	ctc	ctt	gta	gtt	cat	atc	aga	gat	cca	ttc	gat	gga	1344
137	Asn	Phe	Lys	Gln	Leu	Leu	Val	Val	His	Ile	Arg	Asp	Pro	Phe	Asp	Gly	
138		435				440						445					
140	aag	aca	tgc	ggc	ata	tgt	ggt	aac	tat	aat	caa	gat	tca	act	gat	gat	1392
141	Lys	Thr	Cys	Gly	Ile	Cys	Gly	Asn	Tyr	Asn	Gln	Asp	Ser	Thr	Asp	Asp	
142		450				455					460						
144	ttc	ttt	gac	gca	gaa	gga	gca	tgc	gct	cta	acc	ccc	aac	ccc	cca	gga	1440
145	Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly	
146	465				470				475						480		
148	tgt	aca	gag	gaa	cag	aaa	cca	gaa	gct	gag	cga	ctt	tgc	aat	aat	ctc	1488
149	Cys	Thr	Glu	Glu	Gln	Lys	Pro	Glu	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Leu	
150				485				490					495				
152	ttt	gat	tct	tct	atc	gac	gag	aaa	tgt	aat	gtc	tgc	tac	aag	cct	gac	1536
153	Phe	Asp	Ser	Ser	Ile	Asp	Glu	Lys	Cys	Asn	Val	Cys	Tyr	Lys	Pro	Asp	
154			500			505					510						
156	cgg	att	gcc	cga	tgt	atg	tac	gag	tat	tgc	ctg	agg	gga	caa	caa	gga	1584
157	Arg	Ile	Ala	Arg	Cys	Met	Tyr	Glu	Tyr	Cys	Leu	Arg	Gly	Gln	Gln	Gly	
158			515			520					525						
160	ttt	tgt	gac	cat	gct	tgg	gag	ttc	aag	aaa	gaa	tgc	tac	ata	aaa	cat	1632
161	Phe	Cys	Asp	His	Ala	Trp	Glu	Phe	Lys	Lys	Glu	Cys	Tyr	Ile	Lys	His	
162		530				535					540						
164	gga	gac	act	cta	gaa	gta	cca	cct	gaa	tgt	caa	gga	tcc	gtg	agc	aag	1680
165	Gly	Asp	Thr	Leu	Glu	Val	Pro	Pro	Glu	Cys	Gln	Gly	Ser	Val	Ser	Lys	
166	545				550				555						560		
168	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	gag	ctg	gac	1728
169	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	
170			565			570					575						
172	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	ggc	gag	ggc	1776
173	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	
174			580			585					590						
176	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	acc	acc	ggc	1824
177	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	
178			595			600					605						
180	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	ggc	tac	ggc	1872
181	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Gly	Tyr	Gly	
182		610				615					620						
184	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cag	cac	gac	ttc	1920
185	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	
186	625				630				635						640		
188	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	1968
189	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	

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190          645          650          655
192 ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag      2016
193 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
194          660          665          670
196 ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag      2064
197 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
198          675          680          685
200 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac agc      2112
201 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
202          690          695          700
204 cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg      2160
205 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
206 705          710          715          720
208 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc      2208
209 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
210          725          730          735
212 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg      2256
213 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
214          740          745          750
216 ccc gac aac cac tac ctg agc tac cag tcc gcc ctg agc aaa gac ccc      2304
217 Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
218          755          760          765
220 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc      2352
221 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
222          770          775          780
224 ggg atc act ctc ggc atg gac gag ctg tac aag taa      2388
225 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
226 785          790          795
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229 <211> LENGTH: 2502
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234 <221> NAME/KEY: CDS
235 <222> LOCATION: (1)..(2502)
236 <223> OTHER INFORMATION:
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243 aac tgt caa gat gca tgt cct gta gaa gcg gaa ccg cca tca agt aca
244 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr
245          20          25          30
247 cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat
248 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
249          35          40          45
251 acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt
252 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
253          50          55          60

```

invalid <213> response. See item 10
on Euro
summary sheet

48 Seqs 3-9
96 show
this
type of
Euro, too.

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255	gaa	aat	aaa	cca	ggg	aag	aca	tgc	tgt	aga	atg	tgc	cag	tat	gtg	att	240
256	Glu	Asn	Lys	Pro	Gly	Lys	Thr	Cys	Cys	Arg	Met	Cys	Gln	Tyr	Val	Ile	
257	65				70					75					80		
259	gaa	tgc	aga	gta	gaa	gca	gct	ggg	tat	ttt	aga	acg	ttt	tac	ggc	aaa	288
260	Glu	Cys	Arg	Val	Glu	Ala	Ala	Gly	Tyr	Phe	Arg	Thr	Phe	Tyr	Gly	Lys	
261					85					90					95		
263	aga	ttt	aat	ttt	cag	gaa	cct	ggg	aaa	tat	gtg	ctg	gct	agg	gga	acc	336
264	Arg	Phe	Asn	Phe	Gln	Glu	Pro	Gly	Lys	Tyr	Val	Leu	Ala	Arg	Gly	Thr	
265				100					105					110			
267	aag	ggt	ggc	gat	tgg	tct	gta	acc	ctc	acc	atg	gag	aat	cta	gat	gga	384
268	Lys	Gly	Gly	Asp	Trp	Ser	Val	Thr	Leu	Thr	Met	Glu	Asn	Leu	Asp	Gly	
269			115					120					125				
271	cag	aag	gga	gct	gtg	ctg	act	aag	aca	aca	ctg	gag	ggt	gca	gga	gac	432
272	Gln	Lys	Gly	Ala	Val	Leu	Thr	Lys	Thr	Thr	Leu	Glu	Val	Ala	Gly	Asp	
273		130					135					140					
275	gta	ata	gac	att	act	caa	gct	act	gca	gat	cct	atc	aca	ggt	aac	gga	480
276	Val	Ile	Asp	Ile	Thr	Gln	Ala	Thr	Ala	Asp	Pro	Ile	Thr	Val	Asn	Gly	
277	145				150					155					160		
279	gga	gct	gac	cca	ggt	atc	gct	aac	ccg	ttc	aca	att	ggg	gag	gtg	acc	528
280	Gly	Ala	Asp	Pro	Val	Ile	Ala	Asn	Pro	Phe	Thr	Ile	Gly	Glu	Val	Thr	
281				165					170				175				
283	att	gct	ggt	ggt	gaa	ata	ccg	ggc	ttc	aat	atc	aca	gtc	atc	gaa	ttc	576
284	Ile	Ala	Val	Val	Glu	Ile	Pro	Gly	Phe	Asn	Ile	Thr	Val	Ile	Glu	Phe	
285				180					185				190				
287	ttt	aaa	cta	atc	gtg	att	gat	att	ctg	gga	gga	aga	tct	gtg	aga	att	624
288	Phe	Lys	Leu	Ile	Val	Ile	Asp	Ile	Leu	Gly	Gly	Arg	Ser	Val	Arg	Ile	
289			195				200					205					
291	gct	cca	gac	aca	gca	aac	aaa	gga	ctg	ata	tct	ggg	atc	tgt	ggg	aat	672
292	Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn	
293		210				215					220						
295	ctg	gag	atg	aat	gac	gct	gat	gac	ttt	act	aca	gat	gca	gat	cag	ctg	720
296	Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu	
297	225				230					235					240		
299	gcg	atc	caa	ccc	aac	ata	aac	aaa	gag	ttc	gac	ggc	tgc	cca	ttc	tat	768
300	Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr	
301				245					250				255				
303	ggc	aat	cct	tct	gat	atc	gaa	tac	tgc	aaa	ggg	ctg	atg	gag	cca	tac	816
304	Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
305				260					265				270				
307	aga	gct	gta	tgt	cgt	aac	aat	atc	aac	ttc	tac	tat	tac	act	cta	tcc	864
308	Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser	
309			275				280						285				
311	tgt	gcc	ttc	gct	tac	tgt	atg	gga	gga	gaa	gaa	aga	gct	aaa	cac	gtc	912
312	Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val	
313		290				295				300							
315	ctt	ttc	gac	tat	ggt	gag	aca	tgc	gct	gcg	ccg	gaa	acg	aga	gga	acg	960
316	Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
317	305				310					315					320		
319	tgt	ggt	tta	tca	gga	cat	act	ttc	tat	gac	aca	ttc	gac	aaa	gca	aga	1008

VERIFICATION SUMMARY

DATE: 08/04/2006

PATENT APPLICATION: US/10/526,569A

TIME: 12:09:35

Input Set : A:\SAEG129.010APC.txt

Output Set: N:\CRF4\08042006\J526569A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25

L:238 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:236

L:461 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:459 .